

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
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Application Serial Number: 10/519,943  
Source: PU  
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PCT

## RAW SEQUENCE LISTING

DATE: 03/31/2006

PATENT APPLICATION: US/10/519,943

TIME: 15:38:59

Input Set : A:\Final sequence list-12810-00140-US.txt

Output Set: N:\CRF4\03312006\J519943.raw

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3 <110> APPLICANT: Gipmans, Martijn
4     Dahlqvist, Anders
5     Banas, Antoni
6     Stahl, Ulf
7     Wiberg, Eva
8     Lenman, Marit
9     Ronne, Hans
10    Stymme, Sten
12 <120> TITLE OF INVENTION: Use of a gene for increasing the oil content in plants
14 <130> FILE REFERENCE: 12810-00140-US
16 <140> CURRENT APPLICATION NUMBER: US 10/519,943
17 <141> CURRENT FILING DATE: 2004-12-29
18 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/007084
19 <151> PRIOR FILING DATE: 2003-07-03
22 <150> PRIOR APPLICATION NUMBER: EP 02015344.1
23 <151> PRIOR FILING DATE: 2002-07-10
25 <160> NUMBER OF SEQ ID NOS: 2
27 <170> SOFTWARE: PatentIn version 3.3
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 2439
32 <212> TYPE: DNA
33 <213> ORGANISM: Saccharomyces cerevisiae
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (30)..(1994)
39 <400> SEQUENCE: 1
40 cttgtagagg ttaactgggg agtattaca atg atg gca act ccg gct act gat      53
41                               Met Met Ala Thr Pro Ala Thr Asp
42                               1           5
44 ctt att tcc gat aat gat aaa tat aac aag caa tgt ctt tct gat tca      101
45 Leu Ile Ser Asp Asn Asp Lys Tyr Asn Lys Gln Cys Leu Ser Asp Ser
46     10           15           20
48 agt gat agt ggt agt gat gta agc ttt ttt tcc gta aat gaa agc gaa      149
49 Ser Asp Ser Gly Ser Asp Val Ser Phe Phe Ser Val Asn Glu Ser Glu
50  25           30           35           40
52 ggt gaa ttg gat aca atg gag aaa gtg gat acc ttg att gga ggt gca      197
53 Gly Glu Leu Asp Thr Met Glu Lys Val Asp Thr Leu Ile Gly Gly Ala
54           45           50           55
56 aga gtt ata agc aat aaa gta gaa aaa gac agc gat agt gaa caa agg      245
57 Arg Val Ile Ser Asn Lys Val Glu Lys Asp Ser Asp Ser Glu Gln Arg
58     60           65           70
60 gga aga aag aag gaa aca act ggg ccc aat aac tat cat aat tta gaa      293
61 Gly Arg Lys Lys Glu Thr Thr Gly Pro Asn Asn Tyr His Asn Leu Glu

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62	75	80	85	
64	gag aag caa gcg agt gcc att tct ctt gac gct gat gat gaa gat ctc	341		
65	Glu Lys Gln Ala Ser Ala Ile Ser Leu Asp Ala Asp Asp Glu Asp Leu			
66	90	95	100	
68	gat gaa att att tct tat tcg cat gac ggg aac tat gac agc tct cat	389		
69	Asp Glu Ile Ile Ser Tyr Ser His Asp Gly Asn Tyr Asp Ser Ser His			
70	105	110	115	120
72	aaa act ttc tcc ttt tcc tta cca ttt ggt aat aca aat ttc cga tca	437		
73	Lys Thr Phe Ser Phe Ser Leu Pro Phe Gly Asn Thr Asn Phe Arg Ser			
74	125	130	135	
76	agt tca cca tta gcc ata att aaa act gtg ctt ccc aag act cca gat	485		
77	Ser Ser Pro Leu Ala Ile Ile Lys Thr Val Leu Pro Lys Thr Pro Asp			
78	140	145	150	
80	gag ttc atc aaa aag aat cta aga aag aat gag atc aag caa aaa ctg	533		
81	Glu Phe Ile Lys Lys Asn Leu Arg Lys Asn Glu Ile Lys Gln Lys Leu			
82	155	160	165	
84	aaa aaa tca acc tcc att tct tcc ttg gaa gag ata gaa tta ttt aaa	581		
85	Lys Lys Ser Thr Ser Ile Ser Ser Leu Glu Glu Ile Glu Leu Phe Lys			
86	170	175	180	
88	tac gaa agg ggc att gat aat tca agg tta agg gct gtt aaa gaa tct	629		
89	Tyr Glu Arg Gly Ile Asp Asn Ser Arg Leu Arg Ala Val Lys Glu Ser			
90	185	190	195	200
92	ttg gaa atg gat gcc ttg aag aac tcc att aag caa ata aca gca gac	677		
93	Leu Glu Met Asp Ala Leu Lys Asn Ser Ile Lys Gln Ile Thr Ala Asp			
94	205	210	215	
96	cca ttc gac aaa act cat gac gga tat tac cgt tcg cgt tta gaa tct	725		
97	Pro Phe Asp Lys Thr His Asp Gly Tyr Tyr Arg Ser Arg Leu Glu Ser			
98	220	225	230	
100	ata tgg aat gaa ttg gaa gga gat gtc gtt ata atg ggt gga tat cga	773		
101	Ile Trp Asn Glu Leu Glu Gly Asp Val Val Ile Met Gly Gly Tyr Arg			
102	235	240	245	
104	ggt agt gtg cta agg gat gct act act cat aag cga att tgg atc cca	821		
105	Gly Ser Val Leu Arg Asp Ala Thr Thr His Lys Arg Ile Trp Ile Pro			
106	250	255	260	
108	tta aag gca ggt ttg aat atg acg aaa gtc gat tta ttg atc gga cct	869		
109	Leu Lys Ala Gly Leu Asn Met Thr Lys Val Asp Leu Leu Ile Gly Pro			
110	265	270	275	280
112	aat gac gaa gat gaa ctt aaa act cag aag gag att gtc cct gat gga	917		
113	Asn Asp Glu Asp Glu Leu Lys Thr Gln Lys Glu Ile Val Pro Asp Gly			
114	285	290	295	
116	atg cta aca cat ata ggg cct gtt gat atc tct aag agg ttg ata aag	965		
117	Met Leu Thr His Ile Gly Pro Val Asp Ile Ser Lys Arg Leu Ile Lys			
118	300	305	310	
120	agg cta gac gca aat cct aat tta aat gtt cag cag ttt ggc tat gat	1013		
121	Arg Leu Asp Ala Asn Pro Asn Leu Asn Val Gln Gln Phe Gly Tyr Asp			
122	315	320	325	
124	tgg aga tta tcc ttg gac ata tct gcc aag cat tta acg act aaa cta	1061		
125	Trp Arg Leu Ser Leu Asp Ile Ser Ala Lys His Leu Thr Thr Lys Leu			
126	330	335	340	

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128 gag gaa att tac aat aag caa aaa aat aag aag gga ata tac atc att 1109
129 Glu Glu Ile Tyr Asn Lys Gln Lys Asn Lys Lys Gly Ile Tyr Ile Ile
130 345 350 355 360
132 gcc cat tca atg ggc gga ttg gtc gca cat aaa gtg ttg caa gac tgt 1157
133 Ala His Ser Met Gly Gly Leu Val Ala His Lys Val Leu Gln Asp Cys
134 365 370 375
136 act cat ttg ata aga ggt att att tac gtg ggt tcc cca agc caa tgt 1205
137 Thr His Leu Ile Arg Gly Ile Ile Tyr Val Gly Ser Pro Ser Gln Cys
138 380 385 390
140 cca aat att tta ggt cct att agg ttt gga gat gat gtg atg tgg aat 1253
141 Pro Asn Ile Leu Gly Pro Ile Arg Phe Gly Asp Asp Val Met Trp Asn
142 395 400 405
144 aaa cta ttt tca cta aga acc aac ttt ttt atg aga agt agt ttc tat 1301
145 Lys Leu Phe Ser Leu Arg Thr Asn Phe Phe Met Arg Ser Ser Phe Tyr
146 410 415 420
148 ttt cta ccg tta gat ggt aga tgt ttt gtt gac aaa att acc tta gag 1349
149 Phe Leu Pro Leu Asp Gly Arg Cys Phe Val Asp Lys Ile Thr Leu Glu
150 425 430 435 440
152 agg tat gat ttc gat ttt ttt gat aca gat gtt tgg aaa acc ctt ggc 1397
153 Arg Tyr Asp Phe Asp Phe Phe Asp Thr Asp Val Trp Lys Thr Leu Gly
154 445 450 455
156 ttg tca cct ctc gtc aat gag aaa aga gag gaa tca gct cac gaa aaa 1445
157 Leu Ser Pro Leu Val Asn Glu Lys Arg Glu Glu Ser Ala His Glu Lys
158 460 465 470
160 tca aaa tta tta cca agg aaa acg aaa tca gcg ctt tcg ctt aaa gct 1493
161 Ser Lys Leu Leu Pro Arg Lys Thr Lys Ser Ala Leu Ser Leu Lys Ala
162 475 480 485
164 acc cta aac gca act acc aag ttt gtc cta aat gca cct gtt gtt agg 1541
165 Thr Leu Asn Ala Thr Thr Lys Phe Val Leu Asn Ala Pro Val Val Arg
166 490 495 500
168 aat gta gcc ggc aat aat aaa cag gta cca agg gat gtg cct ttc gat 1589
169 Asn Val Ala Gly Asn Asn Lys Gln Val Pro Arg Asp Val Pro Phe Asp
170 505 510 515 520
172 gaa gtc ttc cat aca tct tat gaa gat agc tgt gaa tat tta gcg aga 1637
173 Glu Val Phe His Thr Ser Tyr Glu Asp Ser Cys Glu Tyr Leu Ala Arg
174 525 530 535
176 act tta aaa cgt aca aag aat tat ttg gat agc tta gat tac gac ccg 1685
177 Thr Leu Lys Arg Thr Lys Asn Tyr Leu Asp Ser Leu Asp Tyr Asp Pro
178 540 545 550
180 aac aaa gaa tat cct cca ttg gcc atg gtt tac ggt aac aag gtt ccc 1733
181 Asn Lys Glu Tyr Pro Pro Leu Ala Met Val Tyr Gly Asn Lys Val Pro
182 555 560 565
184 act gtt aga ggt gct aaa gtg aac ggt ata caa gat ata aaa gat ggg 1781
185 Thr Val Arg Gly Ala Lys Val Asn Gly Ile Gln Asp Ile Lys Asp Gly
186 570 575 580
188 aat tat gaa gat ttt tac tat ggt ccg ggc gac ggt gtt gtt cac cat 1829
189 Asn Tyr Glu Asp Phe Tyr Tyr Gly Pro Gly Asp Gly Val Val His His
190 585 590 595 600
192 aaa tgg tta ttg cct gaa cag aga ggc ttt cca gtt gtt tgt aaa atc 1877

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193 Lys Trp Leu Leu Pro Glu Gln Arg Gly Phe Pro Val Val Cys Lys Ile
194          605          610          615
196 gcc agt tct tca ggt cat gtt agc tta atg acg gat ttg aaa tca atg 1925
197 Ala Ser Ser Ser Gly His Val Ser Leu Met Thr Asp Leu Lys Ser Met
198          620          625          630
200 gca aaa gca ttc ata tct atc gtc gac agc gaa aaa gaa gga aga aga 1973
201 Ala Lys Ala Phe Ile Ser Ile Val Asp Ser Glu Lys Glu Gly Arg Arg
202          635          640          645
204 tct cga aca cga act tct tca tgaaaggctt tttattcctt tgtttactat 2024
205 Ser Arg Thr Arg Thr Ser Ser
206          650          655
208 tcatatctgc atttttcttt ttacccaaat tccgcatgct aaaaaaaatc tggcaacgca 2084
210 ccgcgaataa aaataaataa tattttttta tcttttagttg cctaaataact atttatttcg 2144
212 tcaattttac aacctctttt atatacacca ttcgatttcc cacgaagtaa aataataatt 2204
214 ctataaacag atttatctga tatgctcaat ttccctctcc attttcatta ttgtccttct 2264
216 tgctcttcct cgatgtcaaa attaaccttc agccataagc tgcatgctgct acattggggtt 2324
218 aataattgat aaccagaatg actccgttcc atagcgtcta cattatcaat gcattcatct 2384
220 aacaaactct cactaaaatg aaaaccacca acaaattgac agcgaggaca attca 2439
223 <210> SEQ ID NO: 2
224 <211> LENGTH: 655
225 <212> TYPE: PRT
226 <213> ORGANISM: Saccharomyces cerevisiae
228 <400> SEQUENCE: 2
229 Met Met Ala Thr Pro Ala Thr Asp Leu Ile Ser Asp Asn Asp Lys Tyr
230 1 5 10 15
232 Asn Lys Gln Cys Leu Ser Asp Ser Ser Asp Ser Gly Ser Asp Val Ser
233 20 25 30
235 Phe Phe Ser Val Asn Glu Ser Glu Gly Glu Leu Asp Thr Met Glu Lys
236 35 40 45
238 Val Asp Thr Leu Ile Gly Gly Ala Arg Val Ile Ser Asn Lys Val Glu
239 50 55 60
241 Lys Asp Ser Asp Ser Glu Gln Arg Gly Arg Lys Lys Glu Thr Thr Gly
242 65 70 75 80
244 Pro Asn Asn Tyr His Asn Leu Glu Glu Lys Gln Ala Ser Ala Ile Ser
245 85 90 95
247 Leu Asp Ala Asp Asp Glu Asp Leu Asp Glu Ile Ile Ser Tyr Ser His
248 100 105 110
250 Asp Gly Asn Tyr Asp Ser Ser His Lys Thr Phe Ser Phe Ser Leu Pro
251 115 120 125
253 Phe Gly Asn Thr Asn Phe Arg Ser Ser Ser Pro Leu Ala Ile Ile Lys
254 130 135 140
256 Thr Val Leu Pro Lys Thr Pro Asp Glu Phe Ile Lys Lys Asn Leu Arg
257 145 150 155 160
259 Lys Asn Glu Ile Lys Gln Lys Leu Lys Lys Ser Thr Ser Ile Ser Ser
260 165 170 175
262 Leu Glu Glu Ile Glu Leu Phe Lys Tyr Glu Arg Gly Ile Asp Asn Ser
263 180 185 190
265 Arg Leu Arg Ala Val Lys Glu Ser Leu Glu Met Asp Ala Leu Lys Asn
266 195 200 205

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268 Ser Ile Lys Gln Ile Thr Ala Asp Pro Phe Asp Lys Thr His Asp Gly
269      210      215      220
271 Tyr Tyr Arg Ser Arg Leu Glu Ser Ile Trp Asn Glu Leu Glu Gly Asp
272 225      230      235      240
274 Val Val Ile Met Gly Gly Tyr Arg Gly Ser Val Leu Arg Asp Ala Thr
275      245      250      255
277 Thr His Lys Arg Ile Trp Ile Pro Leu Lys Ala Gly Leu Asn Met Thr
278      260      265      270
280 Lys Val Asp Leu Leu Ile Gly Pro Asn Asp Glu Asp Glu Leu Lys Thr
281      275      280      285
283 Gln Lys Glu Ile Val Pro Asp Gly Met Leu Thr His Ile Gly Pro Val
284      290      295      300
286 Asp Ile Ser Lys Arg Leu Ile Lys Arg Leu Asp Ala Asn Pro Asn Leu
287 305      310      315      320
289 Asn Val Gln Gln Phe Gly Tyr Asp Trp Arg Leu Ser Leu Asp Ile Ser
290      325      330      335
292 Ala Lys His Leu Thr Thr Lys Leu Glu Glu Ile Tyr Asn Lys Gln Lys
293      340      345      350
295 Asn Lys Lys Gly Ile Tyr Ile Ile Ala His Ser Met Gly Gly Leu Val
296      355      360      365
298 Ala His Lys Val Leu Gln Asp Cys Thr His Leu Ile Arg Gly Ile Ile
299      370      375      380
301 Tyr Val Gly Ser Pro Ser Gln Cys Pro Asn Ile Leu Gly Pro Ile Arg
302 385      390      395      400
304 Phe Gly Asp Asp Val Met Trp Asn Lys Leu Phe Ser Leu Arg Thr Asn
305      405      410      415
307 Phe Phe Met Arg Ser Ser Phe Tyr Phe Leu Pro Leu Asp Gly Arg Cys
308      420      425      430
310 Phe Val Asp Lys Ile Thr Leu Glu Arg Tyr Asp Phe Asp Phe Phe Asp
311      435      440      445
313 Thr Asp Val Trp Lys Thr Leu Gly Leu Ser Pro Leu Val Asn Glu Lys
314      450      455      460
316 Arg Glu Glu Ser Ala His Glu Lys Ser Lys Leu Leu Pro Arg Lys Thr
317 465      470      475      480
319 Lys Ser Ala Leu Ser Leu Lys Ala Thr Leu Asn Ala Thr Thr Lys Phe
320      485      490      495
322 Val Leu Asn Ala Pro Val Val Arg Asn Val Ala Gly Asn Asn Lys Gln
323      500      505      510
325 Val Pro Arg Asp Val Pro Phe Asp Glu Val Phe His Thr Ser Tyr Glu
326      515      520      525
328 Asp Ser Cys Glu Tyr Leu Ala Arg Thr Leu Lys Arg Thr Lys Asn Tyr
329      530      535      540
331 Leu Asp Ser Leu Asp Tyr Asp Pro Asn Lys Glu Tyr Pro Pro Leu Ala
332 545      550      555      560
334 Met Val Tyr Gly Asn Lys Val Pro Thr Val Arg Gly Ala Lys Val Asn
335      565      570      575
337 Gly Ile Gln Asp Ile Lys Asp Gly Asn Tyr Glu Asp Phe Tyr Tyr Gly
338      580      585      590
340 Pro Gly Asp Gly Val Val His His Lys Trp Leu Leu Pro Glu Gln Arg

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**VERIFICATION SUMMARY**

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